AMENDMENTS TO THE CLAIMS:

Claims 1-16 are canceled without prejudice or disclaimer. Claims 17-32 are added. The following is the status of the above-captioned application as amended.

Claims 1-16 (canceled)

Claim 17 (New). A method of screening enzymes for variants with improved specific activity, comprising the steps of

(i) generating a library of nucleic acid sequences encoding enzyme variants of interest

(ii) providing a nucleic acid sequence encoding an enzyme to be fused with the enzyme in (i)

(iii) fusing nucleic acid sequence encoding enzyme variants in (i) with nucleic acid sequence encoding enzyme in (ii)

(iv) transforming the fused nucleic acid sequence obtained in (iii) into a host cell

(v) culturing host cell in (iv) in order to express the fused enzymes

(vi) sampling each cell culture obtained in (v)

(vii) analyzing samples obtained in (vi) by determining activity ratio of the expressed fused enzymes

(viii) selecting the samples exhibiting the desired activity ratio.

Claim 18 (New). The method of claim 17, wherein the enzymes are fused by means of a linker by fusing nucleic acid sequence encoding enzyme variants in 1(i) with nucleic acid sequence encoding a linker and further with nucleic acid sequence encoding enzyme in 1(ii).

Claim 19 (New). The method of claim 18, wherein the linker consists of 1-40, or 2-20, or 2-10 amino acids.

Claim 20 (New). The method of claim 18, wherein the linker is selected from the group consisting of Poly-Arg, Poly-His, PEPTPEPT, FLAG, Strep-tag II, c-myc, S-, HAT-, 3xFLAG, Calmoludin-binding peptide, Cellulose-binding domain, SBP, Chitin-binding domain, Glutathione S-transferase, Maltose-binding domain.

Claim 21 (New). The method of claim 17, wherein the library is generated by mutating a nucleic acid sequence encoding a wild type enzyme.

Claim 22 (New). The method of claim 17, wherein the library is generated by mutating a nucleic acid sequence encoding a protein engineered enzyme.

Claim 23 (New). The method of claim 17, wherein the enzyme variant in 1(i) is generated by genetic engineering.

Claim 24 (New). The method of claim 21, wherein the enzyme is selected from the group consisting of proteases, cellulases (endoglucanases), β-glucanases, hemicellulases, lipases, peroxidases, laccases, α-amylases, glucoamylases, cutinases, pectinases, reductases, oxidases, phenoloxidases, ligninases, pullulanases, pectate lyases, xyloglucanases, xylanases, pectin acetyl esterases, polygalacturonases, rhamnogalacturonases, pectin lyases, mannanases, pectin methylesterases, cello-biohydrolases, transglutaminases and phytases.

Claim 25 (New). The method of claim 17, wherein the enzyme in 1(ii) is selected from the group consisting of proteases, cellulases (endoglucanases), β-glucanases, hemicellulases, lipases, peroxidases, laccases, α-amylases, glucoamylases, cutinases, pectinases, reductases, oxidases, phenoloxidases, ligninases, pullulanases, pectate lyases, xyloglucanases, xylanases, pectin acetyl esterases, polygalacturonases, rhamnogalacturonases, pectin lyases, mannanases, pectin methylesterases, cello-biohydrolases, transglutaminases and phytases.

Claim 26 (New). The method of claim 17, wherein the host cells in 1(iv) are selected from bacterial cells.

Claim 27 (New). The method of claim 26, wherein the host cells belong to a strain selected from the group consisting of the species *Bacillus alkalophilus*, *Bacillus agaradhaerens, Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus clausii, Bacillus circulans*, *Bacillus coagulans*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus stearothermophilus*, *Bacillus subtilis*, *Bacillus thuringiensis*, *Streptomyces lividans* and *Streptomyces murinus*.

Claim 28 (New). The method of claim 17, wherein the host cells in 1(iv) are selected from fungal cells.

Claim 29 (New). The method of claim 28, wherein the host cells belong to a strain selected from the group consisting of the genera *Acremonium*, *Aspergillus*, *Fusarium*, *Humicola*, *Myceliophthora*, *Neurospora*, *Penicillium*, *Thielavia*, *Tolypocladium*, *Trichoderma*, *Eupenicillium*, *Emericella*, *Eurotium*, *Allomyces*, *Blastocladiella*, *Coelomomyces*, *Achlya, Candida*, *Alternaria*, *Rhizopus* and *Mucor;* preferably the species *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus japonicus*, *Aspergillus niger, Aspergillus nidulans* or *Aspergillus oryzae*.

Claim 30 (New). The method of claim 17, wherein the host cells in 1(iv) are selected from yeast cells.

Claim 31 (New). The method of claim 30, wherein the host cells belong to a strain selected from the group consisting of the genera *Candida*, *Kluyveromyces*, *Saccharomyces*, *Schizosaccharomyces*, *Candida, Pichia*, *Hansehula*, or *Yarrowia*, preferably to the species *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccha-romyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis, Saccharomyces oviformis, Kluyveromyces lactis, Kluyveromyces fragilis, Hansenula polymorpha, Pichia pastoris Yarrowia lipolytica*, *Schizosaccharomyces pombe, Ustilgo maylis, Candida maltose, Pichia guillermondii* and *Pichia methanolio.*

Claim 32 (New). The method of claim 1, wherein the fused enzymes in 1(v) are an extracellular product.